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(54) **A RECOMBINANT YEAST FOR LIGNOCELLULOSE RAW MATERIALS**

REKOMBINANTE HEFE ZUR FERMENTATION VON LIGNOCELLULOSE AUS ROHMATERIAL  
LEVURE RECOMBINEE DESTINEE A DES MATIERES PREMIERES LIGNOCELLULOSIQUES

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(56) References cited:  
**WO-A1-95/13362 WO-A1-97/42307**

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• **DATABASE BIOSIS [Online] TANTIRUNGKIJ MANEE ET AL.: 'Fed-batch fermentation of xylose by a fast-growing mutant of xylose-assimilating recombinant saccharomyces cerevisiae', XP002957085 Database accession no. prev199497222525 & APPLIED MICROBIOLOGY AND BIOTECHNOLOGY**

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**EP 1 282 686 B1**

**Description****FIELD OF INVENTION**

**[0001]** The present invention relates to a method of obtaining yeast for fermentation of lignocellulose raw materials and a recombinant yeast for fermentation of lignocellulose raw materials.

**BACKGROUND TO INVENTION AND DESCRIPTION OF PRIOR ART**

**[0002]** Lignocellulose is the main component of forest product residues and agricultural waste. Lignocellulosic raw materials are mainly composed of cellulose, hemicellulose, and lignin. The cellulose fraction is made up of glucose polymers, whereas the hemicellulose fraction is made up of a mixture of glucose, galactose, mannose, xylose and arabinose polymers. The lignin fraction is a polymer of phenolic compounds. Xylose is found in hardwood and softwood hemicelluloses, whereas arabinose is a component in hemicellulose in certain agricultural crops, such as corn.

**[0003]** The cellulose and hemicellulose fractions can be hydrolyzed to monomeric sugars, which can be fermented to ethanol. Ethanol can serve as an environmentally acceptable liquid fuel for transportation, since carbon dioxide released in the fermentation and combustion processes will be sorbed by growing plants in forests and fields.

**[0004]** The price for lignocellulose-derived ethanol has been estimated by Von Sivers, M., G. Zacchi, L. Olsson, and B. Hahn-Hägerdal. 1994. 'Cost analysis of ethanol production from willow using recombinant *Escherichia coli*.' *Biotechnol. Prog.* 10:555-560. Their calculations were based on the fermentation of all hexose sugars (glucose, galactose and mannose) to ethanol and they estimated that the fermentation of pentose sugars (xylose and arabinose) to ethanol could reduce the price of ethanol by approximately 25%. The microbial conversion of lignocellulosic derived hexoses and pentoses would therefore not only be environmentally acceptable, but could also be cost-effective.

**[0005]** Further, the release of monomeric sugars from lignocellulosic raw materials also release by-products, such as weak acids, furans and phenolic compounds, which are inhibitory to the fermentation process. The commonly used Baker's yeast, *Saccharomyces cerevisiae*, is the only ethanol producing microorganism that is capable of efficiently fermenting non-detoxified lignocellulose hydrolysates (Olsson and Hahn-Hägerdal, "Fermentation of lignocellulosic hydrolysates for ethanol production", *Enzyme Microbial Technol.* 18:312-331, 1996). Particularly, efficient fermenting strains of *Saccharomyces cerevisiae* have been isolated from the fermentation plant at a pulp and paper mill (Lindén et al., "Isolation and characterization of acetic acid-tolerant galactose-fermenting strains of *Saccharomyces cerevisiae* from a

spent sulfite liquor fermentation plant", *Appl. Environ. Microbiol.* 58:1661-1669, 1992).

**[0006]** *Saccharomyces cerevisiae* ferments the hexose sugars glucose, galactose and mannose to provide ethanol, but is unable to ferment the pentose sugars xylose and arabinose due to the lack of one or more enzymatic steps. *Saccharomyces cerevisiae* can ferment xylulose, an isomerization product of xylose, to ethanol (Wang et al., "Fermentation of a pentose by yeasts", *Biochem. Biophys. Res. Commun.* 94:248-254, 1980; Chiang et al., "D-Xylulose fermentation to ethanol by *Saccharomyces cerevisiae*", *Appl. Environ. Microbiol.* 42:284-289, 1981; Senac and Hahn-Hägerdal, "Intermediate metabolite concentrations in xylulose- and glucose-fermenting *Saccharomyces cerevisiae* cells", *Appl. Environ. Microbiol.* 56:120-126, 1990).

**[0007]** In eukaryotic cells, the initial metabolism of xylose is catalyzed by a xylose reductase (XR), which reduces xylose to xylitol, and a xylitol dehydrogenase (XDH), which oxidizes xylitol to xylulose. Xylulose is phosphorylated to xylulose 5-phosphate by a xylulose kinase (XK) and further metabolized through the pentose phosphate pathway and glycolysis to ethanol.

*Saccharomyces cerevisiae* has been genetically engineered to metabolize and ferment xylose. The genes for XR and XDH from the xylose-fermenting yeast *Pichia stipitis* have been expressed in *Saccharomyces cerevisiae* (European Patent to C. Hollenberg, 1991; Hallborn et al., "Recombinant yeasts containing the DNA sequences coding for xylose reductase and xylitol dehydrogenase enzymes", W091/15588; Kötter and Ciriacy, "Xylose fermentation by *Saccharomyces cerevisiae*", *Appl. Microbiol. Biotechnol.* 38:776-783, 1993). The transformants metabolize xylose but do not ferment the pentose sugar to ethanol.

**[0008]** The gene for xylulose kinase (XK) from *Saccharomyces cerevisiae* has been cloned and overexpressed in XR-XDH-expressing transformants of *Saccharomyces cerevisiae* (Deng and Ho, "Xylulokinase activity in various yeasts including *Saccharomyces cerevisiae* containing the cloned xylulokinase gene", *Appl. Biochem. Biotechnol.* 24/25:193-199, 1990; Ho and Tsao, "Recombinant yeasts for effective fermentation of glucose and xylose", W095/13362, 1995; Moniruzzaman et al., "Fermentation of corn fibre sugars by an engineered xylose utilizing a *Saccharomyces* strain", *World J. Microbiol. Biotechnol.* 13:341-346, 1997). These strains have been shown to produce net quantities of ethanol in fermentations of mixtures of xylose and glucose. Using the well established ribosomal integration protocol, the genes have been chromosomally integrated to generate strains that can be used in complex media without selection pressure (Ho and Chen, "Stable recombinant yeasts for fermenting xylose to ethanol", W097/42307; Toon et al., "Enhanced cofermentation of glucose and xylose by recombinant *Saccharomyces* yeast strains in batch and continuous operating modes", *Appl. Biochem. Biotechnol.* 63/65:243-255, 1997).

**[0009]** Although great strides have been made, there exists a need in the art for a method of, and a tool for efficiently fermenting lignocellulose hydrolysates to produce ethanol.

## SUMMARY OF INVENTION

**[0010]** According to the invention, a method for obtaining a recombinant yeast, which ferments lignocellulose raw materials to ethanol, includes introducing DNA into a yeast so as to cause the yeast to have introduced genes encoding xylose reductase, xylitol dehydrogenase and xylulokinase.

**[0011]** In particular the invention relates to a method for obtaining a recombinant, mutated yeast of *Saccharomyces cerevisiae*, which ferments lignocellulose raw materials to ethanol, including introducing DNA into a yeast so as to cause the yeast to have introduced genes encoding xylose reductase obtained from *Pichia stipitis*, xylitol dehydrogenase obtained from *Pichia stipitis* and xylulokinase obtained from *Saccharomyces cerevisiae* and performing a mutation of the strain thus obtained to provide a mutant strain which grows on minimum nutrient containing xylose as sole carbon source.

**[0012]** In a preferred embodiment the *Saccharomyces cerevisiae* strain is *S. cerevisiae* USM21.

**[0013]** In a preferred embodiment the *S. cerevisiae* USM21 strain has been deposited under CBS 102678.

**[0014]** In a preferred embodiment the method includes providing suitable mutants by ethyl methanesulphonate (EMS) treatment.

**[0015]** In a preferred embodiment the lignocellulosic hydrolysate is a non-detoxified hydrolysate.

**[0016]** In a preferred embodiment the lignocellulosic hydrolysate is a detoxified hydrolysate.

**[0017]** In a preferred embodiment the lignocellulosic hydrolysate is a softwood derived hydrolysate.

**[0018]** In a preferred embodiment the lignocellulosic hydrolysate is a hardwood derived hydrolysate.

**[0019]** A further aspect of the invention relates to a recombinant, mutated yeast of *Saccharomyces cerevisiae* containing introduced genes encoding xylose reductase obtained from *Pichia stipitis*, xylitol dehydrogenase obtained from *Pichia stipitis* and xylulokinase obtained from *Saccharomyces cerevisiae* and being able of growing in a minimum nutrient containing xylose as sole carbon source.

**[0020]** In a preferred embodiment *S. cerevisiae* has been deposited under deposition number CBS 102678.

**[0021]** In a preferred embodiment includes mutants produced by ethyl methanesulphonate (EMS) treatment.

**[0022]** In a preferred embodiment the mutant shows a growth rate over its basic strain of more than 30%.

**[0023]** In a preferred embodiment the mutant is deposited under deposition number CBS 102679.

**[0024]** In a preferred embodiment the mutant is deposited under deposition number CBS 102680.

## BRIEF DESCRIPTION OF DRAWINGS

**[0025]** The present invention will now be described by way of examples with reference to the accompanying drawings, in which there is shown in:

**[0026]** **FIGURE 1** is a schematic presentation of the present invention, indicating the physical map of the expression vector Yip2B6 containing the *Pichia stipitis* genes *XYL 1* and *XYL2* encoding XR and XDH, and *Saccharomyces cerevisiae* gene *XK* encoding XK. PGKp = PGK promoter; PGK<sub>t</sub> = PGK terminator.

**[0027]** **FIGURE 2** is a graphical presentation of the present invention, indicating the growth exhibited by two independent xylose-fermenting mutants (XYL125 ■, XYL145 X) and the reference strain (XYLUSM21 λ) in SCX.

## DETAILED DESCRIPTION OF THE DRAWINGS.

**[0028]** According to the invention there is provided a method for providing a microorganism with the capability of efficiently fermenting lignocellulose raw materials to produce ethanol. The method provides the steps of

- transforming the microorganism with a nucleotide sequence comprising genes which encode certain xylose degrading enzymes; and
- a promoter for promoting transcription of these genes in the transformed microorganism and production of these enzymes.

**[0029]** If required to effect synthesis and secretion of these enzymes by the microorganism, the nucleotide sequences can further include suitable leader sequences for these genes.

**[0030]** The microorganism is a yeast strain, and the method provides the yeast strain with the capability of producing at least one of the following lignocellulose utilising enzymes:

- xylose reductase (XR);
- xylitol dehydrogenase (XD); and
- xylulokinase (XK)

**[0031]** The invention further includes a method for fermenting lignocellulosic raw materials with a microorganism which has been transformed into a xylose-utilising microorganism by introducing into the microorganism

- DNA comprising genes which encode xylose utilising enzymes; and
- a promoter for promoting transcription of these genes in the microorganism and production of these enzymes.

**[0032]** The recombinant DNA for use in transforming a microorganism so as to provide it with a capability of fermenting lignocellulose raw materials, said DNA com-

prising of

- genes encoding xylose utilising enzymes; and
- a promoter for promoting transcription of these genes in the transformed microorganism and production of these enzymes.

**[0033]** The xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes which encode the xylose utilising enzymes may be obtained from the following microorganisms:

- Pichia stipitis* (for XR and XD genes)
- Saccharomyces cerevisiae* (for XK gene)

**[0034]** The method for providing a microorganism also encompasses the isolation of mutants on the basis of their ability to grow rapidly on xylose and the characterization of selected strains, said method comprising ethyl methanesulphonate (EMS) treatment.

**[0035]** The mutants are XYL125 and XYL145 and can effectively utilise xylose in the absence of other carbon sources.

**[0036]** It will be appreciated that the recombinant yeasts, mutants, DNA molecules and vectors comprising xylose reductase (XR), xylitol dehydrogenase (XD) and xylulokinase (XK) genes which the present invention provides, are well known to occur in a wide variety of microorganisms and that numerous XR, XD and XK genes have in fact been identified and isolated. The particular source of these genes is not critical to the broad aspects of this invention, as long as the enzymes have occurring XR, XD and XK activity. Further, these genes may be obtained as naturally occurring XR, XD and XK genes, or be modified, or be synthesized by any techniques known in the current state of the art.

**[0037]** The present invention further provides one or more promoters and/or leader sequences for promoting transcription of the genes and production of the enzymes.

**[0038]** A preferred expression vector comprises the xylose reductase- and xylitol dehydrogenase genes from *Pichia stipitis*, and a xylulokinase gene from *Saccharomyces cerevisiae* (together with suitable promoters and possibly leader sequences), which when transformed into *Saccharomyces cerevisiae*, will enable it to utilise xylose.

**[0039]** Legal deposits under the regulations of the Budapest Treaty were made of the *Saccharomyces cerevisiae* transgenic strain (XYLUSM21) as well as the two mutants (XYLUSM125, XYLUSM145) at the Centraal bureau voor Scimmelcultures (CBS) Baarn \$ Delft, The Netherlands. The depositions were made on the 1 st of May, 2000 under the deposition numbers CBS 102678 (XYLUSM21), CBS 102679 (XYLUSM125), and CBS 102680 (XYLUSM145), respectively

**[0040]** Preferred embodiments of the present inventive method will now be illustrated by way of the following non-limiting examples:

## EXAMPLE 1

### Construction of the *Saccharomyces cerevisiae* transgenic strain (XYLUSM21)

**[0041]** *Saccharomyces cerevisiae* (USM21) transformants carrying the xylose reductase (XR) and xylitol dehydrogenase (XDH) genes from the xylose-utilising yeast, *Pichia stipitis*, and the xylulokinase (XK) gene from *Saccharomyces cerevisiae* were constructed. All three genes were placed under control of the PGK promoter-terminator sequences. Competent cells of USM21 were transformed with the linear PstI fragment of Ylp2B6, as substantially showed in Figure 1 in order to integrate a single copy at the locus HIS3 by single crossing-over. Transformed cells were plated on YPX medium.

**[0042]** Xylose-utilising transformants appeared within 4 days at 28°C. Correct integration was verified by Southern analysis and one transformant was retained (strain XYLUSM21).

### Mutagenesis:

**[0043]** Ethyl methanesulfonate (EMS) treatment was carried out according to Ausubel et al. ("Current protocols in molecular biology", Vol. 2nd Chap. 13, 1st ed. John Wiley & Sons, Inc., 1998, Massachusetts).

### Ethyl methanesulfonate (EMS) treatment to obtain two mutants (XYL125, XYL145)

**[0044]** The *Saccharomyces cerevisiae* transgenic strain (XYLUSM21) was treated with ethyl methanesulfonate (EMS) to obtain a 20%, 30%, 40%, and 50% survival rate. The treated cells were washed once with 5% sodium thiosulfate and incubated for 10 minutes at room temperature, then the cells were resuspended in sterile distilled water. All cells were transferred together at the same point in time in 50 ml YPD medium complemented with ampicillin (all in one 50 ml YPD medium liquid culture), and incubated for 24h at 22°C. The culture (XYLUSM21) was transferred 8 times on fresh YPX medium with ampicillin at 24h intervals and the cell xylose-fermentation was monitored in YPX medium Durham tubes at each 24h interval. The 2ml samples which tacked from the culture every 24h were plated on YPX plates supplemented with ampicillin, and then the colonies which showed a faster grow rate were saved.

**[0045]** From the results of the first screening step, two mutants (XYLUSM125, XYLUSM145) with a faster growth rate than that of the reference strain (XYLUSM21) on YPX medium supplemented with ampicillin were selected and their growth were examined. For shake-flask cultures organisms were pre-grown in 50 ml shake-flasks, containing 10 ml of YPD medium and incubated on a rotatory shaker at 150 rpm and 30°C for 16h. These cultures were used to inoculate 500 ml Erlenmeyer flasks, containing 50 ml SCX medium with ampicillin. Cul-

tures were incubated on a rotatory shaker at 150 rpm and 30°C.

[0046] Mutants XYLUSM125 and XYLUSM145 showed a 100% and 75% higher growth rate respectively than that of the *Saccharomyces cerevisiae* transgenic strain (XYLUSM21), as showed in Figure 2. These mutants can effectively use xylose in the absence of other carbon sources.

## EXAMPLE 2

### Strain and Culture media:

[0047] The wine *Saccharomyces cerevisiae* strain USM21 (Kil<sup>+</sup> Gal<sup>+</sup>) (van der Westhuizen and Pretorius, "The value of electrophoretic fingerprinting and karyotyping in wine yeast breeding programmes", Antonie van Leeuwenhoek 61:249-257, 1992; ZA 91/9818) was employed as the recipients for transformation experiments. Yeast strains were grown in complex medium consisting of 1% yeast extract, 2% peptone, 2% glucose (YPD) or 2% xylose (YPX). To perform the growth curves the strains were grown in synthetic complete (SCX) medium containing 0.67% Difco yeast nitrogen base without amino acids supplemented with 2% xylose as sole carbon source. All the media were complemented with ampicillin at a concentration 100 µg/ml to prevent bacterial contamination.

## EXAMPLE 3

### Transformation:

[0048] *Saccharomyces cerevisiae* was carried out according to Gietz et al. ("Studies on the transformation of intact yeast cells by the LiAc/SS-DNA/PEG procedure", Yeast 11: 355-360, 1995).

## EXAMPLE 4

### DNA techniques:

[0049] Plasmid DNA was prepared from *Escherichia. Coli* using the CTAB method (Del Sal et al., "A one-tube plasmid DNA mini-preparation suitable for sequencing", Nucleic Acids Res. 16: 9878, 1988). Standard recombinant DNA techniques were performed essentially as described Sambrook et al. ("Molecular cloning: a laboratory manual, 2nd ed. Cold Spring Harbor Laboratory, Cold Spring Harbor, 1989, NY).

## EXAMPLE 5

### Fermentation

[0050] Fermentation has been carried out in a spruce hydrolysate containing. Thereby XYLUSM125 was grown in 20g/l xylose in minimal medium [Verduyn, C.,

E. Postma, W. A. Scheffers, and J. P. Van Dijken. 1992. Effect of benzoic acid on metabolic fluxes in yeasts: a continuous-culture study on the regulation of respiration and alcoholic fermentation. Yeast 8:501-507.] and establish XYLUSM125 in a continuous culture on 20g/l xylose, using a dilution rate of  $D = 0.1 \text{ h}^{-1}$  (note, aerobic fermentation, adding oxygen). The growth rate obtained on xylose as only carbon source was  $U_{\text{max}} = 0.14\text{-}0.15 \text{ h}^{-1}$  and the biomass yield  $0.4 \text{ g.g}^{-1}$ , thus about 8 g/l biomass on 20g/l xylose as carbon source. When the feed was changed to 20g/l xylose plus 20g/l glucose, the biomass raised to 18 g/l and the surprising result was that only 4-5 g/l xylose remained. This indicates that XYLUSM125 simultaneously utilise 20g/l glucose plus 15-16 g/l xylose in a continuous fermentation at  $D = 0.1 \text{ h}^{-1}$ .

[0051] The experiment was repeated, but this time 20g/l glucose was first fed to establish a steady state in continuous fermentation, all the glucose was utilized with a biomass yield of about 6 g/l. When the feed was changed to 20g/l glucose plus 20g/l xylose, the biomass yield raised to about 14 g/l with all glucose utilized and about 10-12 g/l xylose utilized (thus 8-10 g/l xylose remaining).

## Claims

1. A method for obtaining a recombinant, mutated yeast of *Saccharomyces cerevisiae*, which ferments lignocellulose raw materials to ethanol, including introducing DNA into a yeast so as to cause the yeast to have introduced genes encoding xylose reductase obtained from *Pichia stipitis*, xylitol dehydrogenase obtained from *Pichia stipitis* and xylulokinase obtained from *Saccharomyces cerevisiae* and performing a mutation of the strain thus obtained to provide a mutant strain which grows on minimum nutrient containing xylose as sole carbon source.
2. A method as claimed in claims 1, wherein the *S. cerevisiae* strain has been deposited under deposition number CBS 102678.
3. A method as claimed in claim 1, which includes providing suitable mutants by ethyl methanesulphonate (EMS) treatment.
4. A method as claimed in one or more of the preceding claims wherein the lignocellulosic hydrolysate is a non-detoxified hydrolysate.
5. A method as claimed in one or more of the preceding claims 1-3, wherein the lignocellulosic hydrolysate is a detoxified hydrolysate.
6. A method as claimed in one or more of the preceding claims wherein the lignocellulosic hydrolysate is a softwood derived hydrolysate.



7. A method as claimed in one or more of the preceding claims wherein the lignocellulosic hydrolysate is a hardwood derived hydrolysate.
8. A recombinant, mutated yeast of *Saccharomyces cerevisiae* containing introduced genes encoding xylose reductase obtained from *Pichia stipitis*, xylitol dehydrogenase obtained from *Pichia stipitis* and xylulokinase obtained from *Saccharomyces cerevisiae* and being able of growing in a minimum nutrient containing xylose as sole carbon source.
9. A yeast as claimed in claim 8, which *S. cerevisiae* has been deposited under deposition number CBS 102678.
10. A yeast as claimed in claim 8, which has been mutated by ethyl methanesulphonate (EMS) treatment.
11. A yeast as claimed in claim 10, wherein the mutant is deposited under deposition number CBS 102679.
12. A yeast as claimed in claim 10, wherein the mutant is deposited under deposition number CBS 102680.

#### Patentansprüche

1. Ein Verfahren zum Erhalten einer rekombinanten, mutierten Hefe der *Saccharomyces cerevisiae*, welche Rohmaterialien aus Lignozellulose zu Ethanol fermentiert, eingeschlossen der Einführung von DNA in eine Hefe, um so zu veranlassen, dass die Hefe Gene aufnimmt, die die Xylorereduktase, erhalten vom *Pichia stipitis* und die Xylitoldehydrogenase erhaltend von *Pichia stipitis* und die Xylulokinase erhalten von *Saccharomyces cerevisiae* kodieren, und das Durchführen von Mutationen des so erhaltenen Stammes, um einen mutierten Stamm zu erhalten, der auf einem Minimalnährstoffmedium wächst, welches Xylose als einzige Kohlenstoffquelle enthält.
2. Ein Verfahren wie beansprucht in Anspruch 1, wobei der *S. cerevisiae* Stamm mit der Hinterlegungsnummer CBS 102678 hinterlegt wurde.
3. Ein Verfahren wie beansprucht in Anspruch 1, welches das Bereitstellen geeigneter Mutanten durch eine Ethylmethansulphonat (EMS)-Behandlung einschließt.
4. Ein Verfahren wie in einem oder mehreren der vorangehenden Ansprüche beansprucht, wobei das lignozellulose Hydrolysat ein nicht-entgiftetes Hydrolysat ist.
5. Ein Verfahren wie in einem oder mehreren der vor-

angehenden Ansprüche 1 bis 3 beansprucht, wobei das lignozellulose Hydrolysat ein entgiftetes Hydrolysat ist.

6. Ein Verfahren wie in einem oder mehreren der vorangehenden Ansprüche beansprucht, wobei das lignozellulose Hydrolysat ein aus Weichholz abgeleitetes Hydrolysat ist.
7. Ein Verfahren wie in einem oder mehreren der vorangehenden Ansprüche beansprucht, wobei das lignozellulose Hydrolysat ein aus Hartholz abgeleitetes Hydrolysat ist.
8. Eine rekombinante, mutierte Hefe *Saccharomyces cerevisiae* enthaltend eingeführte Gene, die die Xylorereduktase erhalten aus *Pichia stipitis*, die Xylitoldehydrogenase erhalten aus *Pichia stipitis* und die Xylulokinase erhalten aus *Saccharomyces cerevisiae* kodieren und die in der Lage ist, auf einem Minimalnährstoffmedium zu wachsen, welches Xylose als einzige Kohlenstoffquelle enthält.
9. Eine Hefe wie beansprucht in Anspruch 8, wobei die *S. cerevisiae* mit der Hinterlegungsnummer CBS 102678 hinterlegt wurde.
10. Eine Hefe wie beansprucht in Anspruch 8, welche durch die Ethylmethansulphonat (EMS)-Behandlung mutiert wurde.
11. Eine Hefe wie beansprucht in Anspruch 10, wobei die Mutante mit der Hinterlegungsnummer CBS 102679 hinterlegt wurde.
12. Eine Hefe wie beansprucht in Anspruch 10, wobei die Mutante mit der Hinterlegungsnummer CBS 102680 hinterlegt wurde.

#### Revendications

1. Procédé pour obtenir une levure mutée recombinante de *Saccharomyces cerevisiae*, qui fait fermenter des matières premières lignocellulosiques en éthanol, incluant l'introduction d'ADN dans une levure de manière à amener la levure à avoir des gènes introduits codant la xylose réductase obtenus à partir de *Pichia stipitis*, la xylitol déshydrogénase obtenus à partir de *Pichia stipitis* et la xylulokinase obtenus à partir de *Saccharomyces cerevisiae* et la réalisation d'une mutation de la souche ainsi obtenue pour produire une souche mutante qui se développe sur une substance nutritive minimale contenant du xylose comme seule source de carbone.
2. Procédé selon la revendication 1 où la souche de *S. cerevisiae* a été déposée sous le numéro de dépôt

CBS 102678.

3. Procédé selon la revendication 1 qui inclut la production de mutants appropriés par traitement avec le méthanesulfonate d'éthyle (EMS). 5
4. Procédé selon une ou plusieurs des revendications précédentes où l'hydrolysat lignocellulosique est un hydrolysat non détoxifié. 10
5. Procédé selon une ou plusieurs des revendications 1-3 précédentes où l'hydrolysat lignocellulosique est un hydrolysat détoxifié.
6. Procédé selon une ou plusieurs des revendications précédentes où l'hydrolysat lignocellulosique est un hydrolysat dérivé de bois de conifères. 15
7. Procédé selon une ou plusieurs des revendications précédentes où l'hydrolysat lignocellulosique est un hydrolysat dérivé de bois d'arbres feuillus. 20
8. Levure mutée recombinante de *Saccharomyces cerevisiae* contenant des gènes introduits codant la xylose réductase obtenus à partir de *Pichia stipitis*, la xylitol déshydrogénase obtenus à partir de *Pichia stipitis* et la xylulokinase obtenus à partir de *Saccharomyces cerevisiae* et étant capable de se développer dans une substance nutritive minimale contenant du xylose comme seule source de carbone. 25 30
9. Levure selon la revendication 8, laquelle *S. cerevisiae* a été déposée sous le numéro de dépôt CBS 102678. 35
10. Levure selon la revendication 8 qui a été mutée par traitement avec le méthanesulfonate d'éthyle (EMS).
11. Levure selon la revendication 10 où le mutant est déposé sous le numéro de dépôt CBS 102679. 40
12. Levure selon la revendication 10 où le mutant est déposé sous le numéro de dépôt CBS 102680. 45

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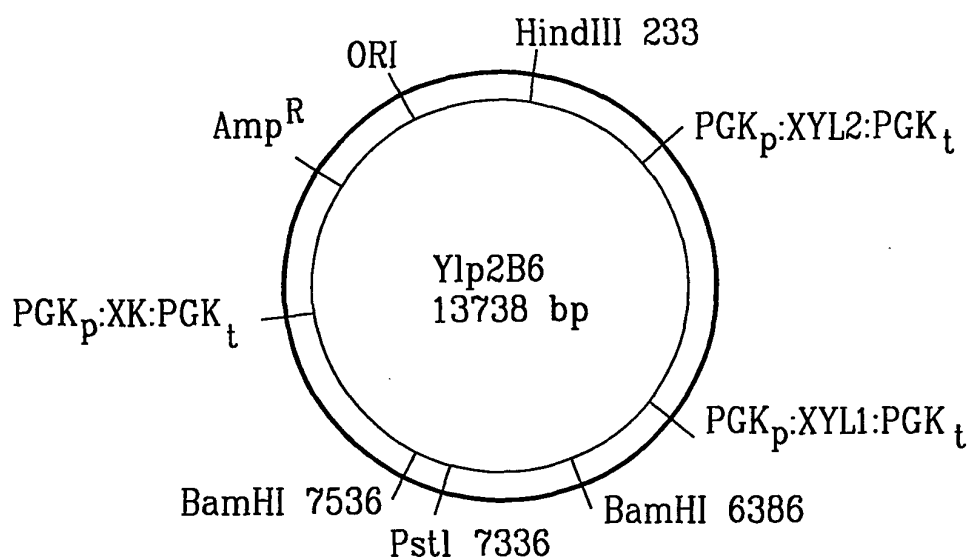


FIG.1

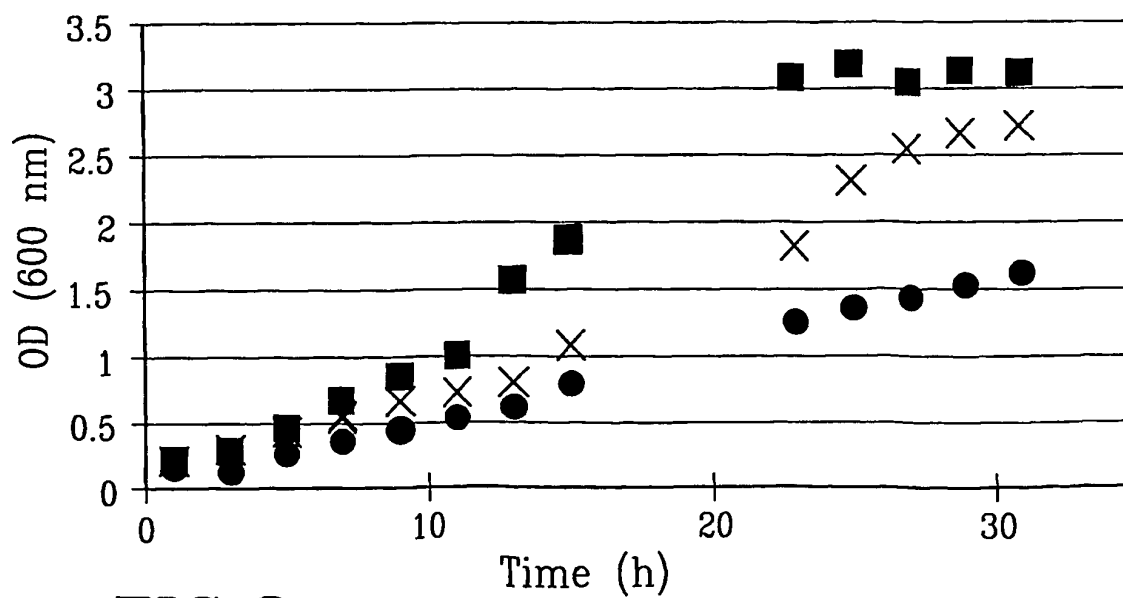


FIG.2

## REFERENCES CITED IN THE DESCRIPTION

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- WO 9513362 A [0008]
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